

=====

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: Thu May 24 14:47:26 EDT 2007

=====

Reviewer Comments:

<150> 08/381,528

<151> 1995-01-31

<160> 9

Number of sequences found are 10.

<210> 10

<211> 1723

<212> PRT

<213> mus musculus

<220>

<223> predicted DEC-205

<400> 3

Change the number at numeric identifier <400>.

Application No: 09925284

Version No: 6.0

Input Set:

Output Set:

Started: 2007-05-24 13:38:18.040

Finished: 2007-05-24 13:38:19.476

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 436 ms

Total Warnings: 6

Total Errors: 1

No. of SeqIDs Defined: 9

Actual SeqID Count: 10

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 252	Calc# of Seq. differs from actual; 9 seqIds defined; count=10

SEQUENCE LISTING

<110> Hawiger, Daniel
 Steinman, Ralph
 Nussenzweig, Michel

<120> Enhanced Antigen Delivery and Modulation
 of the Immune System Therefrom

<130> 600-1-081CONCIP

<140> 09925284

<141> 2001-08-09

<150> 09/925,284

<151> 2001-08-09

<150> 09/586,704

<151> 2000-06-05

<150> 08/381,528

<151> 1995-01-31

<160> 9

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1

atagtttagc ggccgcgata tctcactaac actcattcct gttgaagct 49

<210> 2

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 2

tcttctcaga gagggtgaga ggaccatttc gatcgatcac tcgccggcga tttgata 57

<210> 3

<211> 68

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 3

ctagcgacat ggccaagaag gagacagtct ggaggctcga ggagttcggg aggttcacaa 60
acaggaac 68

<210> 4

<211> 71

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 4

acagacggta gcacagacta tggatttctc cagattaaca gcaggtatta tgacggtagg 60
acatgatagg c 71

<210> 5

<211> 70

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 5

gtctgtgttc ctgtttgtga acctaccgaa ctctcgagc ctccagactg tctccttctt 60
ggccatgtcg 70

<210> 6

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 6

ggccgcctat catgtcctac cgtcataata cctgctgtta atctggagaa taccatagtc 60
tgtgctacc 69

<210> 7

<211> 30

<212> PRT

<213> Homo sapiens

<220>

<223> carboxy terminal DEC-205

<400> 7

Arg	His	Arg	Leu	His	Leu	Ala	Gly	Phe	Ser	Ser	Val	Arg	Tyr	Ala	Gln
1				5					10					15	
Gly	Val	Asn	Glu	Asp	Glu	Ile	Met	Leu	Pro	Ser	Phe	His	Asp		
			20					25					30		

<210> 8
 <211> 25
 <212> PRT
 <213> mus musculus

 <220>
 <223> amino terminal Dec-205

 <400> 8
 Ser Glu Ser Ser Gly Asn Asp Pro Phe Thr Ile Val His Glu Asn Thr
 1 5 10 15
 Gly Lys Cys Ile Gln Pro Leu Phe Asp
 20 25

<210> 9
 <211> 19
 <212> PRT
 <213> mus musculus

<220>
 <223> amino terminal DEC-205

<400> 9
 Ser Glu Ser Ser Gly Asn Asp Pro Phe Thr Ile Val His Glu Asn Thr
 1 5 10 15
 Gly Lys Cys

<210> 10
 <211> 1723
 <212> PRT
 <213> mus musculus

<220>
 <223> predicted DEC-205

<400> 3
 Met Arg Thr Gly Arg Val Thr Pro Gly Leu Ala Ala Gly Leu Leu Leu
 1 5 10 15
 Leu Leu Leu Arg Ser Phe Gly Leu Val Glu Pro Ser Glu Ser Ser Gly
 20 25 30
 Asn Asp Pro Phe Thr Ile Val His Glu Asn Thr Gly Lys Cys Ile Gln
 35 40 45
 Pro Leu Ser Asp Trp Val Val Ala Gln Asp Cys Ser Gly Thr Asn Asn
 50 55 60
 Met Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu Glu Ser
 65 70 75 80
 Gln Lys Cys Leu Gly Leu Asp Ile Thr Lys Ala Thr Asp Asn Leu Arg
 85 90 95
 Met Phe Ser Cys Asp Ser Thr Val Met Leu Trp Trp Lys Cys Glu His
 100 105 110
 His Ser Leu Tyr Thr Ala Ala Gln Tyr Arg Leu Ala Leu Lys Asp Gly
 115 120 125
 Tyr Ala Val Ala Asn Thr Asn Thr Ser Asp Val Trp Lys Lys Gly Gly
 130 135 140
 Ser Glu Glu Asn Leu Cys Ala Gln Pro Tyr His Glu Ile Tyr Thr Arg

145		150		155		160
Asp Gly Asn Ser Tyr	Gly Arg Pro Cys Glu Phe Pro Phe Leu Ile Gly					
	165		170		175	
Glu Thr Trp Tyr His Asp Cys Ile His Asp Glu Asp His Ser Gly Pro						
	180		185		190	
Trp Cys Ala Thr Thr Leu Ser Tyr Glu Tyr Asp Gln Lys Trp Gly Ile						
	195		200		205	
Cys Leu Leu Pro Glu Ser Gly Cys Glu Gly Asn Trp Glu Lys Asn Glu						
	210		215		220	
Gln Ile Gly Ser Cys Tyr Gln Phe Asn Asn Gln Glu Ile Leu Ser Trp						
	225		230		235	
Lys Glu Ala Tyr Val Ser Cys Gln Asn Gln Gly Ala Asp Leu Leu Ser						
	245		250		255	
Ile His Ser Ala Ala Glu Leu Ala Tyr Ile Thr Gly Lys Glu Asp Ile						
	260		265		270	
Ala Arg Leu Val Trp Leu Gly Leu Asn Gln Leu Tyr Ser Ala Arg Gly						
	275		280		285	
Trp Glu Trp Ser Asp Phe Arg Pro Leu Lys Phe Leu Asn Trp Asp Pro						
	290		295		300	
Gly Thr Pro Val Ala Pro Val Ile Gly Gly Ser Ser Cys Ala Arg Met						
	305		310		315	
Asp Thr Glu Ser Gly Leu Trp Gln Ser Val Ser Cys Glu Ser Gln Gln						
	325		330		335	
Pro Tyr Val Cys Lys Lys Pro Leu Asn Asn Thr Leu Glu Leu Pro Asp						
	340		345		350	
Val Trp Thr Tyr Thr Asp Thr His Cys His Val Gly Trp Leu Pro Asn						
	355		360		365	
Asn Gly Phe Cys Tyr Leu Leu Ala Asn Glu Ser Ser Ser Trp Asp Ala						
	370		375		380	
Ala His Leu Lys Cys Lys Ala Phe Gly Ala Asp Leu Ile Ser Met His						
	385		390		395	
Ser Leu Ala Asp Val Glu Val Val Val Thr Lys Leu His Asn Gly Asp						
	405		410		415	
Val Lys Lys Glu Ile Trp Thr Gly Leu Lys Asn Thr Asn Ser Pro Ala						
	420		425		430	
Leu Phe Gln Trp Ser Asp Gly Thr Glu Val Thr Leu Thr Tyr Trp Asn						
	435		440		445	
Glu Asn Glu Pro Ser Val Pro Phe Asn Lys Thr Pro Asn Cys Val Ser						
	450		455		460	
Tyr Leu Gly Lys Leu Gly Gln Trp Lys Val Gln Ser Cys Glu Lys Lys						
	465		470		475	
Leu Arg Tyr Val Cys Lys Lys Lys Gly Glu Ile Thr Lys Asp Ala Glu						
	485		490		495	
Ser Asp Lys Leu Cys Pro Pro Asp Glu Gly Trp Lys Arg His Gly Glu						
	500		505		510	
Thr Cys Tyr Lys Ile Tyr Glu Lys Glu Ala Pro Phe Gly Thr Asn Cys						
	515		520		525	
Asn Leu Thr Ile Thr Ser Arg Phe Glu Gln Glu Phe Leu Asn Tyr Met						
	530		535		540	
Met Lys Asn Tyr Asp Lys Ser Leu Arg Lys Tyr Phe Trp Thr Gly Leu						
	545		550		555	
Arg Asp Pro Asp Ser Arg Gly Glu Tyr Ser Trp Ala Val Ala Gln Gly						
	565		570		575	
Val Lys Gln Ala Val Thr Phe Ser Asn Trp Asn Phe Leu Glu Pro Ala						
	580		585		590	
Ser Pro Gly Gly Cys Val Ala Met Ser Thr Gly Lys Thr Leu Gly Lys						
	595		600		605	

Trp	Glu	Val	Lys	Asn	Cys	Arg	Ser	Phe	Arg	Ala	Leu	Ser	Ile	Cys	Lys	610	615	620
Lys	Val	Ser	Glu	Pro	Gln	Glu	Pro	Glu	Glu	Ala	Ala	Pro	Lys	Pro	Asp	625	630	635
Asp	Pro	Cys	Pro	Glu	Gly	Trp	His	Thr	Phe	Pro	Ser	Ser	Leu	Ser	Cys	645	650	655
Tyr	Lys	Val	Phe	His	Ile	Glu	Arg	Ile	Val	Arg	Lys	Arg	Asn	Trp	Glu	660	665	670
Glu	Ala	Glu	Arg	Phe	Cys	Gln	Ala	Leu	Gly	Ala	His	Leu	Pro	Ser	Phe	675	680	685
Ser	Arg	Arg	Glu	Glu	Ile	Lys	Asp	Phe	Val	His	Leu	Leu	Lys	Asp	Gln	690	695	700
Phe	Ser	Gly	Gln	Arg	Trp	Leu	Trp	Ile	Gly	Leu	Asn	Lys	Arg	Ser	Pro	705	710	715
Asp	Leu	Gln	Gly	Ser	Trp	Gln	Trp	Ser	Asp	Arg	Thr	Pro	Val	Ser	Ala	725	730	735
Val	Met	Met	Glu	Pro	Glu	Phe	Gln	Gln	Asp	Phe	Asp	Ile	Arg	Asp	Cys	740	745	750
Ala	Ala	Ile	Lys	Val	Leu	Asp	Val	Pro	Trp	Arg	Arg	Val	Trp	His	Leu	755	760	765
Tyr	Glu	Asp	Lys	Asp	Tyr	Ala	Tyr	Trp	Lys	Pro	Phe	Ala	Cys	Asp	Ala	770	775	780
Lys	Leu	Glu	Trp	Val	Cys	Gln	Ile	Pro	Lys	Gly	Ser	Thr	Pro	Gln	Met	785	790	795
Pro	Asp	Trp	Tyr	Asn	Pro	Glu	Arg	Thr	Gly	Ile	His	Gly	Pro	Pro	Val	805	810	815
Ile	Ile	Glu	Gly	Ser	Glu	Tyr	Trp	Phe	Val	Ala	Asp	Pro	His	Leu	Asn	820	825	830
Tyr	Glu	Glu	Ala	Val	Leu	Tyr	Cys	Ala	Ser	Asn	His	Ser	Phe	Leu	Ala	835	840	845
Thr	Ile	Thr	Ser	Phe	Thr	Gly	Leu	Lys	Ala	Ile	Lys	Asn	Lys	Leu	Ala	850	855	860
Asn	Ile	Ser	Gly	Glu	Glu	Gln	Lys	Trp	Trp	Val	Lys	Thr	Ser	Glu	Asn	865	870	875
Pro	Ile	Asp	Arg	Tyr	Phe	Leu	Gly	Ser	Arg	Arg	Arg	Leu	Trp	His	His	885	890	895
Phe	Pro	Met	Thr	Phe	Gly	Asp	Glu	Cys	Leu	His	Met	Ser	Ala	Lys	Thr	900	905	910
Trp	Leu	Val	Asp	Leu	Ser	Lys	Arg	Ala	Asp	Cys	Asn	Ala	Lys	Leu	Pro	915	920	925
Phe	Ile	Cys	Glu	Arg	Tyr	Asn	Val	Ser	Ser	Leu	Glu	Lys	Tyr	Ser	Pro	930	935	940
Asp	Pro	Ala	Ala	Lys	Val	Gln	Cys	Thr	Glu	Lys	Trp	Ile	Pro	Phe	Gln	945	950	955
Asn	Lys	Cys	Phe	Leu	Lys	Val	Asn	Ser	Gly	Pro	Val	Thr	Phe	Ser	Gln	965	970	975
Ala	Ser	Gly	Ile	Cys	His	Ser	Tyr	Gly	Gly	Thr	Leu	Pro	Ser	Val	Leu	980	985	990
Ser	Arg	Gly	Glu	Gln	Asp	Phe	Ile	Ile	Ser	Leu	Leu	Pro	Glu	Met	Glu	995	1000	1005
Ala	Ser	Leu	Trp	Ile	Gly	Leu	Arg	Trp	Thr	Ala	Tyr	Glu	Arg	Ile	Asn	1010	1015	1020
Arg	Trp	Thr	Asp	Asn	Arg	Glu	Leu	Thr	Tyr	Ser	Asn	Phe	His	Pro	Leu	1025	1030	1035
Leu	Val	Gly	Arg	Arg	Leu	Ser	Ile	Pro	Thr	Asn	Phe	Phe	Asp	Asp	Glu	1045	1050	1055
Ser	His	Phe	His	Cys	Ala	Leu	Ile	Leu	Asn	Leu	Lys	Lys	Ser	Pro	Leu			

	1060		1065		1070
Thr Gly Thr Trp Asn Phe Thr Ser Cys Ser Glu Arg His Ser Leu Ser					
1075		1080		1085	
Leu Cys Gln Lys Tyr Ser Glu Thr Glu Asp Gly Gln Pro Trp Glu Asn					
1090		1095		1100	
Thr Ser Lys Thr Val Lys Tyr Leu Asn Asn Leu Tyr Lys Ile Ile Ser					
1105		1110		1115	1120
Lys Pro Leu Thr Trp His Gly Ala Leu Lys Glu Cys Met Lys Glu Lys					
	1125		1130		1135
Met Arg Leu Val Ser Ile Thr Asp Pro Tyr Gln Gln Ala Phe Leu Ala					
	1140		1145		1150
Val Gln Ala Thr Leu Arg Asn Ser Ser Phe Trp Ile Gly Leu Ser Ser					
	1155		1160		1165
Gln Asp Asp Glu Leu Asn Phe Gly Trp Ser Asp Gly Lys Arg Leu Gln					
	1170		1175		1180
Phe Ser Asn Trp Ala Gly Ser Asn Glu Gln Leu Asp Asp Cys Val Ile					
1185		1190		1195	1200
Leu Asp Thr Asp Gly Phe Trp Lys Thr Ala Asp Cys Asp Asp Asn Gln					
	1205		1210		1215
Pro Gly Ala Ile Cys Tyr Tyr Pro Gly Asn Glu Thr Glu Glu Glu Val					
	1220		1225		1230
Arg Ala Leu Asp Thr Ala Lys Cys Pro Ser Pro Val Gln Ser Thr Pro					
	1235		1240		1245
Trp Ile Pro Phe Gln Asn Ser Cys Tyr Asn Phe Met Ile Thr Asn Asn					
	1250		1255		1260
Arg His Lys Thr Val Thr Pro Glu Glu Val Gln Ser Thr Cys Glu Lys					
1265		1270		1275	1280
Leu His Pro Lys Ala His Ser Leu Ser Ile Arg Asn Glu Glu Glu Asn					
	1285		1290		1295
Thr Phe Val Val Glu Gln Leu Leu Tyr Phe Asn Tyr Ile Ala Ser Trp					
	1300		1305		1310
Val Met Leu Gly Ile Thr Tyr Glu Asn Asn Ser Leu Met Trp Phe Asp					
	1315		1320		1325
Lys Thr Ala Leu Ser Tyr Thr His Trp Arg Thr Gly Arg Pro Thr Val					
	1330		1335		1340
Lys Asn Gly Lys Phe Leu Ala Gly Leu Ser Thr Asp Gly Phe Trp Asp					
1345		1350		1355	1360
Ile Gln Ser Phe Asn Val Ile Glu Glu Thr Leu His Phe Tyr Gln His					
	1365		1370		1375
Ser Ile Ser Ala Cys Lys Ile Glu Met Val Asp Tyr Glu Asp Lys His					
	1380		1385		1390
Asn Gly Thr Leu Pro Gln Phe Ile Pro Tyr Lys Asp Gly Val Tyr Ser					
	1395		1400		1405
Val Ile Gln Lys Lys Val Thr Trp Tyr Glu Ala Leu Asn Ala Cys Ser					
	1410		1415		1420
Gln Ser Gly Gly Glu Leu Ala Ser Val His Asn Pro Asn Gly Lys Leu					
1425		1430		1435	1440
Phe Leu Glu Asp Ile Val Asn Arg Asp Gly Phe Pro Leu Trp Val Gly					
	1445		1450		1455
Leu Ser Ser His Asp Gly Ser Glu Ser Ser Phe Glu Trp Ser Asp Gly					
	1460		1465		1470
Arg Ala Phe Asp Tyr Val Pro Trp Gln Ser Leu Gln Ser Pro Gly Asp					
	1475		1480		1485
Cys Val Val Leu Tyr Pro Lys Gly Ile Trp Arg Arg Glu Lys Cys Leu					
	1490		1495		1500
Ser Val Lys Asp Gly Ala Ile Cys Tyr Lys Pro Thr Lys Asp Lys Lys					
1505		1510		1515	1520

Leu	Ile	Phe		His	Val	Lys	Ser	Ser	Lys	Cys	Pro	Val	Ala	Lys	Arg	Asp
					1525					1530						1535
Gly	Pro	Gln	Trp	Val	Gln	Tyr	Gly	Gly	His	Cys	Tyr	Ala	Ser	Asp	Gln	
					1540				1545						1550	
Val	Leu	His	Ser	Phe	Ser	Glu	Ala	Lys	Gln	Val	Cys	Gln	Glu	Leu	Asp	
		1555						1560					1565			
His	Ser	Ala	Thr	Val	Val	Thr	Ile	Ala	Asp	Glu	Asn	Glu	Asn	Lys	Phe	
		1570					1575				1580					
Val	Ser	Arg	Leu	Met	Arg	Glu	Asn	Tyr	Asn	Ile	Thr	Met	Arg	Val	Trp	
1585					1590					1595					1600	
Leu	Gly	Leu	Ser	Gln	His	Ser	Leu	Asp	Gln	Ser	Trp	Ser	Trp	Leu	Asp	
					1605				1610						1615	
Gly	Leu	Asp	Val	Thr	Phe	Val	Lys	Trp	Glu	Asn	Lys	Thr	Lys	Asp	Gly	
					1620				1625					1630		
Asp	Gly	Lys	Cys	Ser	Ile	Leu	Ile	Ala	Ser	Asn	Glu	Thr	Trp	Arg	Lys	
		1635						1640				1645				
Val	His	Cys	Ser	Arg	Gly	Tyr	Ala	Arg	Ala	Val	Cys	Lys	Ile	Pro	Leu	
		1650					1655				1660					
Ser	Pro	Asp	Tyr	Thr	Gly	Ile	Ala	Ile	Leu	Phe	Ala	Val	Leu	Cys	Leu	
1665						1670				1675					1680	
Leu	Gly	Leu	Ile	Ser	Leu	Ala	Ile	Trp	Phe	Leu	Leu	Gln	Arg	Ser	His	
					1685				1690						1695	
Ile	Arg	Trp	Thr	Gly	Phe	Ser	Ser	Val	Arg	Tyr	Glu	His	Gly	Thr	Asn	
					1700				1705					1710		
Glu	Asp	Glu	Val	Met	Leu	Pro	Ser	Phe	His	Asp						
		1715						1720								